

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L. et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSEE: Dr. Kathleen L. Horwath
  - (B) STREET: Department of Biological Sciences, Binghamton University
  - (C) CITY: Binghamton
  - (D) STATE: New York
  - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
  - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
  - (B) COMPUTER: IBM AT/ATX compatible
  - (C) OPERATING SYSTEM: Windows 95/98
  - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
  - (A) APPLICATION NUMBER: 60210446
  - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
  - (A) NAME: Mark Levy, Attorney-at-Law
  - (B) REGISTRATION NUMBER: 29,188
  - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
  - (A) TELEPHONE: 607-722-6600
  - (B) TELEFAX: 607-724-2207

09876796-060701

## (2) INFORMATION FOR SEQ. ID NO: 1

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Peptide

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (v) FRAGMENT TYPE: N-terminal fragment

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

## (ix) FEATURES:

- (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val  
 1                      5                      10                      15

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## (2) INFORMATION FOR SEQ. ID NO: 2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*  
 (B) INDIVIDUAL/ISOLATE: none  
 (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA  
 (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC 36  
 Met Lys Leu Leu  
 -15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG 81  
 Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu  
 -10 -5 1

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT 126  
 Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys  
 5 10 15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC 171  
 Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg  
 20 25 30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT 216  
 Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe  
 35 40 45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG 261  
 Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val  
 50 55 60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC 306  
 Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn  
 65 70 75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA 351  
 Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg  
 80 85 90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG 396  
 Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met  
 95 100 105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA 439  
 Lys Asn Lys Pro Lys Phe Ser Pro Val Asp \*  
 110 115

CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTC 489

TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG 539

CGGCCGCGGG CCCATCGTTT TCCACCC 566

## (2) INFORMATION FOR SEQ. ID NO: 3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val  
 -15 -10 -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys  
 1 5 10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala  
 15 20 25 30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe  
 35 40 45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val  
 50 55 60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu  
 65 70 75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val  
 80 85 90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro  
 95 100 105 110

Lys Phe Ser Pro Val Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 4

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys  
 1                      5                      10                      15  
 Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn  
                     20                      25                      30  
 Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val  
                     35                      40                      45  
 Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp  
                     50                      55                      60  
 Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr  
 65                      70                      75                      80  
 Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu  
                     85                      90                      95  
 Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe  
                     100                      105                      110  
 Ser Pro Val Asp \*  
                     115

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## (2) INFORMATION FOR SEQ. ID NO: 5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTG TTTGACTGAA TTTTGACAAT AAAGGTAATA 455  
 Ile Asp \*  
 115

TCGTTATGTA AAAAAAAAAA AAAAAA 481

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## (2) INFORMATION FOR SEQ. ID NO: 6

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

## (ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46  
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
-15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91  
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
-5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136  
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG 316  
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
100 105 110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455  
Ile Asp \*  
115

TCGTTATGAA AAAAAAAAAA AAAAAAAAAA 482

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## (2) INFORMATION FOR SEQ. ID NO: 7

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 8

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 12.84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
 1 5 10 15  
 Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
 20 25 30  
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
 35 40 45  
 Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
 50 55 60  
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
 65 70 75 80  
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
 85 90 95  
 Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 Pro Ile Asp \*  
 115

09826796-060701

## (2) INFORMATION FOR SEQ. ID NO: 9

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455  
 Ile Asp \*  
 115

TCGTTATGTA AAAAAAAAAA AAAAAA 481

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## (2) INFORMATION FOR SEQ. ID NO: 10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Clone 3.4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 11

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Clone 3.4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
 1 5 10 15  
 Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
 20 25 30  
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
 35 40 45  
 Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
 50 55 60  
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
 65 70 75 80  
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
 85 90 95  
 Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 Pro Ile Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 12

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

## (ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455  
 Ile Asp \*  
 115

TCGTTATGAA AAAAAAAAAA AAAAAAAAAA 482

09876543210

## (2) INFORMATION FOR SEQ. ID NO: 13

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
                   -15                  -10                  -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
           1                              5                              10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
  15                              20                              25                              30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
                               35                              40                              45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
                               50                              55                              60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
           65                              70                              75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
           80                              85                              90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
  95                              100                              105                              110

Phe Ser Pro Ile Asp \*  
                               115

J09876796-060704

## (2) INFORMATION FOR SEQ. ID NO: 14

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature protein for Clone 3.9

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
 1 5 10 15  
 Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
 20 25 30  
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
 35 40 45  
 Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
 50 55 60  
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
 65 70 75 80  
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
 85 90 95  
 Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 Pro Ile Asp \*  
 115

09876796-060701

```
(2) INFORMATION FOR SEQ. ID NO: 15
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 481 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: cDNA to mRNA
  (iii) HYPOTHETICAL: no
  (iv) ANTI-SENSE: no
  (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Tenebrio molitor
      (B) INDIVIDUAL/ISOLATE: none
      (C) CELL TYPE: fat body and whole organism
  (vii) IMMEDIATE SOURCE:
      (A) LIBRARY: cDNA
      (B) CLONE: 7.5
  (ix) FEATURES
      (D) OTHER INFORMATION: Non-his-tagged, Signal plus
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
```

RB125 SEQ



## (2) INFORMATION FOR SEQ. ID NO: 16

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

098796.060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1b:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-45 -40 -35

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT 231  
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276  
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser  
1 5 10

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321  
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp  
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG 366  
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411  
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala  
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456  
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val  
60 65 70

GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501  
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546  
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys  
90 95 100

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA 595  
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

TTTGA CTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA 645

AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT 681

T02090-9679360

(i) SEQUENCE CHARACTERISTICS:

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | -55 | His | His | His | His | -50 | His | Ser | Ser | Gly | Leu | Val | Pro |     |
| Arg | Gly | Ser | -40 | His | Met | Ala | Ser | Met | Thr | Gly | Gly | Gln | Gln | Met | Gly | Arg |
| Gly | Ser | Glu | -25 | Phe | Ala | Arg | Ala | Lys | Met | Lys | Leu | Leu | Leu | Cys | Phe | Ala |
| Phe | Ala | Ala | -10 | Ile | Val | Ile | Gly | Ala | Gln | Ala | Leu | Thr | Asp | Glu | Gln | Ile |
| Gln | Lys | Arg |     | Asn | Lys | Ile | Ser | Lys | Glu | Cys | Gln | Gln | Val | Ser | Gly | Val |
| Ser | Gln | Glu | 25  | Thr | Ile | Asp | Lys | Val | Arg | Thr | Gly | Val | Leu | Val | Asp | Asp |
| Pro | Lys | Met | 40  | Lys | Lys | His | Val | Leu | Cys | Phe | Ser | Lys | Lys | Thr | Gly | Val |
| Ala | Thr | Glu | 55  | Ala | Gly | Asp | Thr | Asn | Val | Glu | Val | Leu | Lys | Ala | Lys | Leu |
| Lys | His | Val |     | Ala | Ser | Asp | Glu | Glu | Val | Asp | Lys | Ile | Val | Gln | Lys | Cys |
| Val | Val | Lys |     | Lys | Ala | Thr | Pro | Glu | Glu | Thr | Ala | Tyr | Asp | Thr | Phe | Lys |
| Cys | Ile | Tyr | 105 | Asp | Ser | Lys | Pro | Asp | Phe | Ser | Pro | Ile | Asp | *   |     |     |

## (2) INFORMATION FOR SEQ. ID NO: 18

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*  
 (B) INDIVIDUAL/ISOLATE: none  
 (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA  
 (B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
 Met Gly Ser Ser His His His His His His Ser  
 -30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
 Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
 -20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186  
 Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
 -5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231  
 Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
 10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT 276  
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
 25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321  
 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr  
 40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
 Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
 55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411  
 Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
 70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
 85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
 Pro Ile Asp \*  
 115

## (2) INFORMATION FOR SEQ. ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

```
(ix) FEATURES
```

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
          -15                          -10                              -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 20
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 682 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.3
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal Plus

09876796-050701

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG														50	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser														96	
-55 -50															
AGC	GGC	CTG	GTG	CCG	CGC	GGC	AGC	CAT	ATG	GCT	AGC	ATG	ACT	GGT	141
Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	
-45 -40 -35															
GGA	CAG	CAA	ATG	GGT	CGC	GGA	TCC	GAA	TTC	GCA	CGA	GCA	AAA	ATG	186
Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Glu	Phe	Ala	Arg	Ala	Lys	Met	
-30 -25 -20															
AAA	CTC	CTC	TTG	TGC	TTT	GCT	TTC	GCC	GCC	ATC	GTC	ATC	GGA	GCT	231
Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala	Ile	Val	Ile	Gly	Ala	
-15 -10 -5															
CAG	GCT	CTC	ACC	GAC	GAA	CAG	ATA	CAG	AAA	AGG	AAC	AAG	ATC	AGC	276
Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	
1 5 10															
AAA	GAA	TGC	CAG	CAG	GTG	TCC	GGA	GTG	TCC	CAA	GAG	ACG	ATC	GAC	321
Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	
15 20 25															
AAA	GTC	CGC	ACA	GGT	GTG	TTG	GTC	GAT	GAT	CCC	AAA	ATG	AAG	AAG	366
Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	
30 35 40															
CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	ACT	GGA	GTG	GCA	ACC	GAA	GCC	411
His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	
45 50 55															
GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	GCC	AAG	CTG	AAG	CAT	GTG	456
Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	
60 65 70															
GCC	AGC	GAC	GAA	GAA	GTG	GAC	AAG	ATC	GTG	CAG	AAG	TGC	GTG	GTC	501
Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	Val	Val	
75 80 85															
AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	TAT	GAC	ACC	TTC	AAG	TGT	546
Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	Cys	
90 95 100															
ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	CCT	ATT	GAT	TAA	TTGTTTTGTA		595
Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro	Ile	Asp	*			
105 110 115															
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA														645	
AAAAAAAACTC GAGCAACCACC ACCACCACCA CTGAGAT														682	

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(B) CLONE: 2.3

(D) OTHER INFORMATION: Precursor Protein with His-tag



- (2) INFORMATION FOR SEQ. ID NO: 22
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 543 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.3
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal minus
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186  
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
-5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231  
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT 276  
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321  
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr  
40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC 411  
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456  
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
Pro Ile Asp \*  
115

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

```
(ix)FEATURES
```

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
          -15                          -10                              -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 777 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 13.17
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

09876543210-050704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-65 -60 -55

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-50 -45 -40

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile  
-35 -30 -25

CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC 231  
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser  
-20 -15 -10

CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT 276  
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile  
-5 1 5

GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA 321  
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly  
10 15 20

GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG 366  
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu  
25 30 35

GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC 411  
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn  
40 45 50

GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG 456  
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu  
55 60 65

AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG 501  
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu  
70 75 80

AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG 546  
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu  
85 90 95

ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG 595  
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys  
100 105 110

TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG 643  
Phe Ser Pro Val Asp \*  
115

TGTGCTTTAC ATATAAAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA 693

AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT 743

TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT 777

T02090" 96492860

## (2) INFORMATION FOR SEQ. ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile  
-25 -20 -15 -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile  
-5 1 5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val  
10 15 20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp  
25 30 35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu  
40 45 50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val  
55 60 65 70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys  
75 80 85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe  
90 95 100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp \*

## (2) INFORMATION FOR SEQ. ID NO: 26

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-20 -15 -10

GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA 186  
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys  
-5 1 5

CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG 231  
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser  
10 15 20

CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT 276  
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp  
25 30 35

CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT 321  
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly  
40 45 50

CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG 366  
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu  
55 60 65

AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC 411  
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile  
70 75 80

ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG 456  
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val  
85 90 95

TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA 501  
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser  
100 105 110

CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
Pro Val Asp \*  
115

(i) SEQUENCE CHARACTERISTICS:

- ```
(ix)FEATURES
```

(D) OTHER INFORMATION: Mature Protein with His-tag

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys  
1 5 10 15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg  
20 25 30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys  
35 40 45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val  
50 55 60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu  
65 70 75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu  
80 85 90 95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys  
100 105 110

Phe Ser Pro Val Asp \*  
115

## (2) INFORMATION FOR SEQ. ID NO: 28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*  
(B) INDIVIDUAL/ISOLATE: none  
(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA  
(B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus



|                                                                |            |                                             |            |            |           |     |    |
|----------------------------------------------------------------|------------|---------------------------------------------|------------|------------|-----------|-----|----|
|                                                                | TTGTTAGCGG | ATGGAATTCC                                  | CTCGTAGGGG | ATAATTTTGT | TACTTTAAG |     | 50 |
| AAGGAGATAT                                                     | ACC        | ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC |            |            |           | 96  |    |
|                                                                |            | Met Gly Ser Ser His His His His His His Ser | -55        |            | -50       |     |    |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT    |            |                                             |            |            |           | 141 |    |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly    | -45        |                                             | -40        |            | -35       |     |    |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG    |            |                                             |            |            |           | 186 |    |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met    | -30        |                                             | -25        |            | -20       |     |    |
| AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT    |            |                                             |            |            |           | 231 |    |
| Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala    | -15        |                                             | -10        |            | -5        |     |    |
| CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC    |            |                                             |            |            |           | 276 |    |
| Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser    | 1          |                                             | 5          |            | 10        |     |    |
| AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC    |            |                                             |            |            |           | 321 |    |
| Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp    | 15         |                                             | 20         |            | 25        |     |    |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG    |            |                                             |            |            |           | 366 |    |
| Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys    | 30         |                                             | 35         |            | 40        |     |    |
| CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC    |            |                                             |            |            |           | 411 |    |
| His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala    | 45         |                                             | 50         |            | 55        |     |    |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG    |            |                                             |            |            |           | 456 |    |
| Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val    | 60         |                                             | 65         |            | 70        |     |    |
| GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC    |            |                                             |            |            |           | 501 |    |
| Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val    | 75         |                                             | 80         |            | 85        |     |    |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT    |            |                                             |            |            |           | 546 |    |
| Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val    | 90         |                                             | 95         |            | 100       |     |    |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA |            |                                             |            |            |           | 595 |    |
| Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *              | 105        |                                             | 110        |            | 115       |     |    |
| TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA         |            |                                             |            |            |           | 645 |    |
| AAAAAACTCG AGCACCAACCA CCACCACCAC TGAGAT                       |            |                                             |            |            |           | 681 |    |

## (2) INFORMATION FOR SEQ. ID NO: 29

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Precursor protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

```
Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                      110                      115
```

- (2) INFORMATION FOR SEQ. ID NO: 30
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
  - (B) CLONE: 3.4
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186  
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
-5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231  
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276  
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321  
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr  
40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411  
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456  
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
85 90 95

TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
Pro Ile Asp \*  
115



## (2) INFORMATION FOR SEQ. ID NO: 32

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal plus

09876796-060701

|                                                                                                           |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
|-----------------------------------------------------------------------------------------------------------|-----|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG                                                    |     |  |  |  |  |  |  |  |  |  |  |  |  | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC<br>Met Gly Ser Ser His His His His His His Ser |     |  |  |  |  |  |  |  |  |  |  |  |  | 96  |
| -55 -50                                                                                                   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT                                               | 141 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| -45 -40 -35                                                                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG                                               | 186 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| -30 -25 -20                                                                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT                                               | 231 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| -15 -10 -5                                                                                                |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC                                               | 276 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 1 5 10                                                                                                    |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC                                               | 321 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 15 20 25                                                                                                  |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG                                               | 366 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 30 35 40                                                                                                  |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC                                               | 411 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 45 50 55                                                                                                  |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG                                               | 456 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 60 65 70                                                                                                  |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC                                               | 501 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 75 80 85                                                                                                  |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT                                               | 546 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 90 95 100                                                                                                 |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA                                            | 595 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *                                                         |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 105 110 115                                                                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA                                                    |     |  |  |  |  |  |  |  |  |  |  |  |  | 645 |
| AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT                                                                 |     |  |  |  |  |  |  |  |  |  |  |  |  | 682 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(C) STRANDEDNESS: si

(D) TOPOLOGY: linear

MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55                      60                      65                      70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

## (2) INFORMATION FOR SEQ. ID NO: 34

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50  
 AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
 Met Gly Ser Ser His His His His His His Ser  
 -30 -25  
 AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
 Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
 -20 -15 -10  
 GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG 186  
 Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
 -5 1 5  
 AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG 231  
 Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val  
 10 15 20  
 TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276  
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
 25 30 35  
 GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT 321  
 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr  
 40 45 50  
 GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
 Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
 55 60 65  
 GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC 411  
 Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
 70 75 80  
 GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
 85 90 95  
 TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
 Pro Ile Asp \*  
 115



## (2) INFORMATION FOR SEQ. ID NO: 35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
                   -30                  -25                  -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
                   -15                  -10                  -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
                   1                  5                  10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
   15                  20                  25                  30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
                   35                  40                  45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
                   50                  55                  60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
                   65                  70                  75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
   80                  85                  90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
   95                  100                  105                  110

Phe Ser Pro Ile Asp \*  
                   115

104090"96492860

- (2) INFORMATION FOR SEQ. ID NO: 36
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 681 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 7.5
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

05875796-060701

RB125 SEQ

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(C) STRANDEDNESS: si

(D) TOPOLOGY: linear

MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE

(A) ORGANISM: *Tenebrio molitor*

(C) CELL TYPE: fat body and

IMMEDIATE SOURCE:

(B) CLONE: 7.5

## FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

## (2) INFORMATION FOR SEQ. ID NO: 38

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 76  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

## (2) INFORMATION FOR SEQ. ID NO: 40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG

24

09876795-050704

- (2) INFORMATION FOR SEQ. ID NO: 41
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

09876796-050701



## (2) INFORMATION FOR SEQ. ID NO: 42

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA

24

T02090-9649660

## (2) INFORMATION FOR SEQ. ID NO: 43

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAAC TGAGC TCGCC 25

F07090" 56794860

## (2) INFORMATION FOR SEQ. ID NO: 44

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
|-----|------|-----|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|
| GGC | ACG  | GAG | CA   | AAA  | ATG  | AAA  | CTC  | CTC  | TTG  | TGC  | TTT  | GCN  | TTC  | GCC  | GCC | 46  |
|     |      |     |      |      | Met  | Lys  | Leu  | Leu  | Leu  | Cys  | Phe  | Ala  | Phe  | Ala  | Ala |     |
|     |      |     |      |      |      |      | -15  |      |      |      |      |      |      |      | -10 |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| ATC | GTC  | ATC | GGA  | GCT  | CAG  | GCT  | CTC  | ACC  | GAY  | GAA  | CAG  | ATA  | CAG  | AAA  |     | 91  |
| Ile | Val  | Ile | Gly  | Ala  | Gln  | Ala  | Leu  | Thr  | Asp  | Glu  | Gln  | Ile  | Gln  | Lys  |     |     |
|     |      |     | -5   |      |      |      | 1    |      |      |      | 5    |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| AGG | AAC  | AAG | ATC  | AGC  | AAA  | GAR  | TGC  | CAG  | CAG  | GNG  | TCC  | GGA  | GTG  | TCC  |     | 136 |
| Arg | Asn  | Lys | Ile  | Ser  | Lys  | Glu  | Cys  | Gln  | Gln  | Val  | Ser  | Gly  | Val  | Ser  |     |     |
|     | 10   |     |      |      |      | 15   |      |      |      |      | 20   |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| CAA | GAG  | ACG | ATC  | GAC  | AAA  | GTC  | CGC  | ACA  | GGT  | GTC  | TTG  | GTC  | GAY  | GAT  |     | 181 |
| Gln | Glu  | Thr | Ile  | Asp  | Lys  | Val  | Arg  | Thr  | Gly  | Val  | Leu  | Val  | Asp  | Asp  |     |     |
|     | 25   |     |      |      |      | 30   |      |      |      |      | 35   |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| CCC | AAA  | ATG | AAG  | AAG  | CAC  | GTC  | CTC  | TGC  | TTC  | TCG  | AAG  | ARA  | ACT  | GGA  |     | 226 |
| Pro | Lys  | Met | Lys  | Lys  | His  | Val  | Leu  | Cys  | Phe  | Ser  | Lys  | Lys  | Thr  | Gly  |     |     |
|     | 40   |     |      |      |      | 45   |      |      |      |      | 50   |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| GTG | GCA  | ACC | GAA  | GCC  | GGA  | GAC  | ACC  | AAT  | GTG  | GAG  | GTA  | CTC  | AAA  | GCC  |     | 271 |
| Val | Ala  | Thr | Glu  | Ala  | Gly  | Asp  | Thr  | Asn  | Val  | Glu  | Val  | Leu  | Lys  | Ala  |     |     |
|     | 55   |     |      |      |      | 60   |      |      |      |      | 65   |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| AAG | CTG  | AAG | CAT  | GTG  | GCC  | AGC  | GAC  | GAA  | GAR  | GTG  | GAC  | AAG  | ATC  | GTG  |     | 316 |
| Lys | Leu  | Lys | His  | Val  | Ala  | Ser  | Asp  | Glu  | Glu  | Val  | Asp  | Lys  | Ile  | Val  |     |     |
|     | 70   |     |      |      |      | 75   |      |      |      |      | 80   |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| CAG | AAG  | TGC | GTG  | GTC  | AAG  | AAG  | GCC  | ACA  | CCA  | GAG  | GAA  | ACG  | GCT  | TAT  |     | 361 |
| Gln | Lys  | Cys | Val  | Val  | Lys  | Lys  | Ala  | Thr  | Pro  | Glu  | Glu  | Thr  | Ala  | Tyr  |     |     |
|     | 85   |     |      |      |      | 90   |      |      |      |      | 95   |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| GAC | ACC  | TTC | AAG  | NNT  | ATT  | TAC  | GAC  | AGT  | AAA  | CCT  | GAT  | TTC  | TCT  | CCT  |     | 406 |
| Asp | Thr  | Phe | Lys  | Cys  | Ile  | Tyr  | Asp  | Ser  | Lys  | Pro  | Asp  | Phe  | Ser  | Pro  |     |     |
|     | 100  |     |      |      |      | 105  |      |      |      |      | 110  |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| ATT | GAT  | TAA | TTG  | TTTT | TGTA | TTTG | RCT  | GAA  | TTTT | GACA | AT   | AAAG | GT   | ANTA |     | 455 |
| Ile | Asp  | *   |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
|     | 115  |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
|     |      |     |      |      |      |      |      |      |      |      |      |      |      |      |     |     |
| TCG | TTAT | GNA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA | AAAA |     | 481 |

## (2) INFORMATION FOR SEQ. ID NO: 45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

## (ix) FEATURES

- (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13-17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

|             |            |        |     |            |            |            |             |     |     |     |     |     |     |     |     |
|-------------|------------|--------|-----|------------|------------|------------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGCANRRNNNN | AAR        | ATG    | AAR | YTN        | CTC        | TNN        | TGY         | YTN | RYN | TYC | NYC | RYY |     | 46  |     |
|             | Met        | Lys    | Leu | Leu        | Leu        | Cys        | Phe         | Ala | Phe | Ala | Ala |     |     |     |     |
|             |            |        |     |            |            | -15        |             |     |     |     |     |     |     |     |     |
| NTN         | NTN        | RTC    | RNA | GYT        | CAG        | GCT        | CTN         | ACC | GAN | GNA | CAR | ATN | NAG | AAA | 91  |
| Ile         | Val        | Ile    | Gly | Ala        | Gln        | Ala        | Leu         | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|             |            |        | -5  |            |            |            | 1           |     |     |     | 5   |     |     |     |     |
| NNG         | AAC        | AAG    | ATC | AGC        | AAA        | RAR        | TGY         | CAR | NAN | GNR | NNY | GGA | GTG | TCN | 136 |
| Arg         | Asn        | Lys    | Ile | Ser        | Lys        | Glu        | Cys         | Gln | Gln | Val | Ser | Gly | Val | Ser |     |
|             | 10         |        |     |            |            | 15         |             |     |     |     | 20  |     |     |     |     |
| CAA         | GAG        | AYN    | ATN | RNC        | AAA        | GYT        | CGC         | ANN | GGT | GNC | TNG | GNN | GAY | GAT | 181 |
| Gln         | Glu        | Thr    | Ile | Asp        | Lys        | Val        | Arg         | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|             | 25         |        |     |            |            | 30         |             |     |     |     | 35  |     |     |     |     |
| CCY         | AAA        | NTG    | AAR | NRN        | CAN        | GTG        | YTY         | TGC | NTN | NCN | ARG | ARN | RCY | GGN | 226 |
| Pro         | Lys        | Met    | Lys | Lys        | His        | Val        | Leu         | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|             | 40         |        |     |            |            | 45         |             |     |     |     | 50  |     |     |     |     |
| NTG         | GCN        | ACN    | GAA | NCN        | GGA        | GAN        | RYN         | RNN | GTN | GAN | GTR | YTN | ARR | GNN | 271 |
| Val         | Ala        | Thr    | Glu | Ala        | Gly        | Asp        | Thr         | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|             | 55         |        |     |            |            | 60         |             |     |     |     | 65  |     |     |     |     |
| AAG         | NTG        | ARG    | NAN | GTN        | RCY        | RRC        | AAC         | GAC | GAA | GAR | RYN | GAN | AAR | ATC | 316 |
| Lys         | Leu        | Lys    | His | Val        | Ala        | Ser        | Asn         | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|             | 70         |        |     |            |            | 75         |             |     |     |     | 80  |     |     |     |     |
| RTN         | NAN        | AAG    | TGC | GYN        | GTC        | AAG        | ARR         | GNV | ACN | NYN | GAR | GAR | ACG | GYN | 361 |
| Val         | Gln        | Lys    | Cys | Val        | Val        | Lys        | Lys         | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|             | 85         |        |     |            |            | 90         |             |     |     |     | 95  |     |     |     |     |
| TNY         | RAY        | ACY    | TTC | AAR        | NNT        | RTY        | NNN         | RAN | ARY | AAR | CCN | RAN | TTC | TCN | 406 |
| Tyr         | Asp        | Thr    | Phe | Lys        | Cys        | Ile        | Tyr         | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|             | 100        |        |     |            |            | 105        |             |     |     |     | 110 |     |     |     |     |
| CCN         | RTT        | GAT    | TRA | NYNNYYNNNA | YTNGNNNRNR | NTTYRANAAT | AAAGNNNNNTN |     |     |     |     |     |     |     | 458 |
| Pro         | Ile        | Asp    | *   |            |            |            |             |     |     |     |     |     |     |     |     |
|             | 115        |        |     |            |            |            |             |     |     |     |     |     |     |     |     |
| TNRTNNNRNA  | AAAAAAAAAA | AAAAAA |     |            |            |            |             |     |     |     |     |     |     |     | 484 |

- (2) INFORMATION FOR SEQ. ID NO: 46
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v)
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

NAA GAN RYN ATN RNN ARA GYY CGC ANN GGT GNC TNG GNN GAY GAY 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYN GRN 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN 316  
 Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile  
 70 75 80

NYN NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN 361  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
 85 90 95

TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN CCN RNN TYY TYN 406  
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110

CNN RYT RNT TRN NYNNNNNNNN YNNGNNNRNR NTTYRANAAT AAAGNNNYTN 458  
 Pro Ile Asp \*  
 115

TNRTNNNRNA AAAAAAAAAA AAAAAA 484

09876796-060704

## (2) INFORMATION FOR SEQ. ID NO: 47

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGC        | NNR        | NNNN   | AAR | ATG        | AAR        | YTN        | CTC        | YNN | TGY | YTN | RYN | YYY | NYN | RYY | 46  |
|            |            |        | Met | Lys        | Leu        | Leu        | Leu        | Cys | Phe | Ala | Phe | Ala | Ala |     |     |
|            |            |        |     |            |            |            | -15        |     |     |     |     |     |     |     | -10 |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NTN        | NTN        | RYC    | NNR | RYN        | YAN        | GCT        | NTN        | ACG | NAN | RNA | NNN | NNN | NAG | NNR | 91  |
| Ile        | Val        | Ile    | Gly | Ala        | Gln        | Ala        | Leu        | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |            | -5     |     |            |            |            | 1          |     |     |     | 5   |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNG        | NNY        | NAR    | NNC | AGC        | RNN        | RNN        | TGY        | NAR | NNN | GNR | NNY | GGA | GTR | TCN | 136 |
| Arg        | Asn        | Lys    | Ile | Ser        | Lys        | Glu        | Cys        | Gln | Gln | Glu | Ser | Gly | Val | Ser |     |
|            | 10         |        |     |            |            | 15         |            |     |     |     | 20  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NAA        | GAN        | NYN    | NTN | RNN        | ARR        | GYY        | CGC        | ANN | NGT | GNN | NNR | GNN | GAY | GAY | 181 |
| Gln        | Glu        | Thr    | Ile | Asp        | Lys        | Val        | Arg        | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            | 25         |        |     |            |            | 30         |            |     |     |     | 35  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| CCY        | AAA        | NTG    | AAR | NNN        | CAN        | YYY        | YTY        | TGC | NTN | NYN | ARG | RNN | YYY | GRN | 226 |
| Pro        | Lys        | Met    | Lys | Lys        | His        | Val        | Leu        | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            | 40         |        |     |            |            | 45         |            |     |     |     | 50  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NTN        | RYN        | RNN    | GNN | NNN        | GGN        | GAN        | NYN        | NNN | NYN | GAN | NNN | NTN | ARR | RNN | 271 |
| Val        | Ala        | Thr    | Glu | Ala        | Gly        | Asp        | Thr        | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            | 55         |        |     |            |            | 60         |            |     |     |     | 65  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| AAR        | NTN        | ANG    | NRN | NNN        | NNN        | RNN        | RNN        | NNN | RAR | RAR | RYN | RRN | RRN | NTN | 316 |
| Lys        | Leu        | Lys    | His | Val        | Ala        | Ser        | Asn        | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|            | 70         |        |     |            |            | 75         |            |     |     |     | 80  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NYN        | NNN        | ARN    | NNN | NNN        | NNN        | NNG        | ARN        | RNN | NYN | NNN | NAR | NNN | NNN | NNN | 361 |
| Val        | Gln        | Lys    | Cys | Val        | Val        | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|            | 85         |        |     |            |            | 90         |            |     |     |     | 95  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNN        | RAN        | NYN    | YYN | AAN        | NNN        | NNY        | NNN        | RRN | ANN | ARN | YCN | NNN | TNN | NNN | 406 |
| Tyr        | Asp        | Thr    | Phe | Lys        | Cys        | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|            | 100        |        |     |            |            | 105        |            |     |     |     | 110 |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| CNN        | NYN        | RNN    | TRN | NNNNNNNNNN | YNNRNNNNNN | NNNNNNNAAT | AAANNNNNNN |     |     |     |     |     |     |     | 458 |
| Pro        | Ile        | Asp    | *   |            |            |            |            |     |     |     |     |     |     |     |     |
|            | 115        |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNNNNNNNNA | AAAAAAAAAA | AAAAAA |     |            |            |            |            |     |     |     |     |     |     |     | 484 |

(2) INFORMATION FOR SEQ. ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE:

(ix) FEATURES

(D) OTHER INFORMATION: Genral Consensus of Clones, B1, B2 and AFP-3

**SECRET**

RB125 SEQ